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OM protein - protein search, using sw model

Run on: March 17, 2001; 20:25:53 ; Search time 77.81 seconds

(without alignments)

254.443 Million cell updates/sec

**title:** Perfect score: US-09-456-306-2

**Sequence:** 1 MAHSAEQEQLIDLEAQGVKKR.....GGVAMIDLARSNIRNIPF 579

**Scoring table:** BLOSUM62

**Gapop 10.0 , Gapext 0.5**

**Searched:** 268485 seqs, 34193/95 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

**Post processing:** Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

**Database :**

1: /cgn2\_2/gcdata/geneseq/geneseq/geneseq/AAI1980.DAT:\*

2: /cgn2\_2/gcdata/geneseq/geneseq/geneseq/AAI1982.DAT:\*

3: /cgn2\_2/gcdata/geneseq/geneseq/geneseq/AAI1983.DAT:\*

4: /cgn2\_2/gcdata/geneseq/geneseq/geneseq/AAI1984.DAT:\*

5: /cgn2\_2/gcdata/geneseq/geneseq/geneseq/AAI1985.DAT:\*

6: /cgn2\_2/gcdata/geneseq/geneseq/AAI1986.DAT:\*

7: /cgn2\_2/gcdata/geneseq/geneseq/AAI1987.DAT:\*

8: /cgn2\_2/gcdata/geneseq/geneseq/AAI1988.DAT:\*

9: /cgn2\_2/gcdata/geneseq/geneseq/AAI1989.DAT:\*

10: /cgn2\_2/gcdata/geneseq/geneseq/AAI1990.DAT:\*

11: /cgn2\_2/gcdata/geneseq/geneseq/AAI1991.DAT:\*

12: /cgn2\_2/gcdata/geneseq/geneseq/AAI1992.DAT:\*

13: /cgn2\_2/gcdata/geneseq/geneseq/AAI1993.DAT:\*

14: /cgn2\_2/gcdata/geneseq/geneseq/AAI1994.DAT:\*

15: /cgn2\_2/gcdata/geneseq/geneseq/AAI1995.DAT:\*

16: /cgn2\_2/gcdata/geneseq/geneseq/AAI1996.DAT:\*

17: /cgn2\_2/gcdata/geneseq/geneseq/AAI1997.DAT:\*

18: /cgn2\_2/gcdata/geneseq/geneseq/AAI1998.DAT:\*

19: /cgn2\_2/gcdata/geneseq/geneseq/AAI1999.DAT:\*

20: /cgn2\_2/gcdata/geneseq/geneseq/AAI2000.DAT:\*

21: /cgn2\_2/gcdata/geneseq/geneseq/AAI2001.DAT:\*

**RESULT 1**

P80477 standard: protein; 592 AA.

ID P80477; XX AC P80477; XX DT 06-NOV-1990 (first entry) XX DE Pyruvate oxidase. XX KW Pyruvate oxidase; ADP; ATP; Pyruvic acid. XX PN EP274425-A. XX PD 13-JUL-1988. XX PF 06-JAN-1988; 88EP-0300073. XX PR 15-MAY-1987; 87JP-0118161. XX PR 15-MAY-1987; 87JP-0000903. XX PA (TOXN ) TOYO JOZO KK.,

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	560.5	18.8	592	P80477
2	537.5	18.0	570	R09316
3	530.5	17.8	570	R05793
4	522.5	17.5	562	W22459
5	517.5	17.3	562	P81153
6	515	17.3	548	W22460
7	514	17.2	548	R88842
8	514	17.2	548	R8681
9	514	17.2	548	W13731
10	496.5	16.6	669	R28618
11	495.5	16.6	669	R2789
12	495.5	16.6	669	R88617

**Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.**

CC  
XX It is produced by recombinant means.  
SQ Sequence 592 AA;

Query Match 18 8%; Score 560 5; DB 9; Length 592;  
Best Local Similarity 29.7%; Pred. No. 1.1e-39;  
Matches 154; Conservative 109; Mismatches 235; Indels 21; Gaps 10;  
OY |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:  
Db 16 iesgadtyqipsgtqslsmdangeeenvkf:qykheevgamaavangs:kgfqnlgvt 75  
OY 71 ASCCGPNTHLIGQJYDHSRNGAKVLAASHIPSQAQGSTFFQETPEIIFKESSGYCEAV 130  
Db 76 gsgppgashlingydaamndipwalgssrprqrelmdafqelqnqnpmyhdhavynrv 135  
OY 131. NGGQGERILHHAQSTMAGKGVSVVWVGDIAK-EDADGTYNSTISGGTPVFPDP 189  
Db 136 ayaeqlpkivdearalmaikrgavavlepgdfakveidhdqwyssanslrkyapiapaq 195  
OY 190 EAALALVEAINNAKSVTLCAGAGVNRARAVLEAKIKSPIGHALGGKQYIQHNPFE-- 247  
Db 195 diakavellnkskpivqasgqthgpgavkarkip-ittgkutefwfdeal 253  
OY 248 VGMGLLGYGACVDAVSNEADLLILGTPYSD---FLPKDNAQVQDINGAHIGRRTV 303  
Db 254 tgstyrvgykpanetileadtviflagskfpsevegtfknvdntiqidipamlgkhrha 313  
OY 304 KYPVTDGVAVIENLPHKREKTRSRFLDRMLK--AHERKLSSVETYTHNVEHVPIH 361  
Db 314 dvailgdglaidealinkdavveawtaknkuianreyimlet--keegdlqfjq 370  
OY 362 EYVSVILNELADKAVFTWDGMCNVWHARYE-NPEGRTRDFEVGSFRHGTMANALPHAIG 420  
Db 371 vyna--innhadealaysidvgnsntqtsirhlmptkm--wrtspifmtmgialppg 426  
OY 421 AQSVDRNRQVIAMCGDGGIIGMLIGCELLTVKHLQPLKAVFVNNSLGMVKLEMVEGQPE 480  
Db 427 akntrypdqgwniigdafsntypdvtvrvnypinvfnsteyafiknkyedtnkhl 486  
OY 481 FGTQHEEVNAEIAAAAGIKSVRITDPKKVREQIAEALA 519  
Db 487 fgvstfdvdyakiadeaqgakgftvsriedmdrvnaeava 525  
RESULT 2  
R0916 ID R0916 standard; Protein; 570 AA.  
XX R0916;  
XX 15-FEB-1993 (first entry)  
XX DE Pyruvate oxidase (P178S, A425V).  
XX POD; mutation; decarboxylation; assay.  
XX Synthetic.  
FH Key Location/Qualifiers  
FH 178 Misc-difference  
FT /label= mutation  
FT /note= "Pro -> Ser; at least one of wild-type  
FT Pro178 and Ala425 is exchanged for Ser178 and Val425"  
FT Misc-difference 425  
FT /label= mutation  
FT /note= "Ala -> Val; at least one of wild-type  
FT Pro178 and Ala425 is exchanged for Ser178 and Val425"  
XX DE3833601-A.

XX 05-APR-1990.  
PD XX 03-OCT-1988; 88DE-3833601.  
PF XX (BOEF ) BOEHRINGER MANNHEIM GMBH.  
PT XX Mollerling H, Schumacher G;  
DR XX WPI; 1990-108586/15.  
PS XX N-PSDB; Q08597.  
PT XX New stable, mutated forms of pyruvate oxidase - having specific  
PT aminoacid substitutions, useful as assay reagents, are encoded in  
new DNA.  
XX PS Claim 2; Page 5; 10Pp; German.  
XX The DNA sequence of wild-type POD, given in 003827, may be mutated so  
CC that at least 178-Pro and/or 425-Ala of the encoded pod are exchanged.  
CC This may be achieved by mutation of nucleotides 532, 533, 534, 1273,  
CC 1274 and/or 1225.  
CC For example, the sequence given below comprises mutations of  
nucleotides 532 and 1274 from C to T, resulting in exchange from  
CC 178-Pro to Ser and 425-Ala to Val.  
CC The mutated pyruvate oxidase (POD) decarboxylates pyruvate with  
CC formation of H<sub>2</sub>O<sub>2</sub> and is active without addn. of FAD, thiamine  
CC pyrophosphate and divalent metal ions. It is more stable (esp. in  
CC presence of salts and at alkaline pH) than wild-type enzyme, and is  
CC better suited for assay of pyruvate, or pyruvate generating reactions.  
XX SQ Sequence 570 AA;  
Query Match 18 0%; Score 537 5; DB 11; Length 570;  
Best Local Similarity 26.6%; Pred. No. 9.8e-38;  
Matches 142; Conservative 113; Mismatches 227; Indels 51; Gaps 9;  
OY 9 LIDTLEAQWKRIGLQYGLGSLNPIYD--RQSDLEWVHRNEAAFAAGAESLITGL 66  
Db 17 vikvleawg�hlygipggsinsindalsaerdrhyqvrheevgamaaadakltgi 76  
OY 67 AVCAASCPEGNTLHQJYDHSRNGAKVLAASHIPSQAQGSTFFQETHEPEIIFKECSY 126  
Db 77 gvcfgsagqgthmnglydaedhgvplaligqfgtgmmndfqgennenpnyadv 136  
OY 127 CEMVNGEGERILHHAQSTMAGKGVSVVWVGDIAKEDAGDGTYSNSTISSEPMVFP 186  
Db 137 nvtavaatlpvhideaarrayangqvavqipdwqg----isaerpl- 184  
OY 187 DPTEAAALVEAINNAKSVTLCAGAGVNRARAVLEAKIKSPIGHALGGKQYIQHNP 246  
Db 185 -----yygikarkakgeleqisktiklkipinstyptakglwadrypa 224  
OY 247 EVGMSGLLGYGACVDAVSNEADLLILGTPYSD---FLPKDNAQVQDINGAHIGRRT 302  
Db 225 Ylgasnrvaqkpanetileadqadvlvggnypfaeskfrtryflqidipamlgkhrha 284  
OY 303 KYPVTDGVAVIENLPHKREKTRSRFLDRMLK--AHERKLSSVETYTHNVEHV 359  
Db 285 tdiavladactktailaqgvservestpwwqanlankvwraylasled----kqepl 338  
OY 360 HPEVYASVINELAQDAVFTWDGMCNVWHARYE-NPEGRTRDFEVGSFRHGTMANALP 419  
Db 339 qayqylarvakiadealaysidvgdinhanhriktspsnrhitsnl-fatmygipgai 397  
OY 420 GAQSVDRNRQVIAMCGDGGIIGMLIGCELLTVKHLQPLKAVFVNNSLGMVKLEMVEGQ 479  
Db 398 aaklnhyperqyqfnlagggasntqdlvrvqyqipwvivwthcqyqfikdqedtnq 457  
OY 480 EF-GTIDHEEVNAEIAAAAGIKSVRITDPKKVRE--QLAELAYPGPVLDIV 529

Db	458	dfiygefndidfskladgvhmgqravnkreqlpdfeqakalaqhepvlidav	510
Db	225	ylgsanvaqkpanaalaqadvlfvgnnypfaevaskaftrfyqidopaklkrh	284
Qy	303	VKYPYGDVANTENLPHWKEKTRSFQFLRML--KAHERKLSSVETVYHNEKHPV	359
ID	R05793	standard; Protein: 570 AA.	
XX	R05793;		
AC			
DT	15-FEB-1993	(first entry)	
XX			
DE	Pyruvate oxidase (wild-type).		
XX			
KW	POD; mutation; decarboxylation; assay.		
OS	Synthetic.		
XX			
PN	DE3833601-A.		
XX			
PD	05-APR-1990.		
XX			
PF	88DE-3833601.		
XX			
PR	03-OCT-1988;	88DE-3833601.	
XX			
PA	(BOEFL) BOEHRINGER MANNHEIM GMBH.		
XX			
PI	Mollerling H, Schumacher G;		
XX			
DR	WPI: 1990-108586/15.		
XX			
PT	New stable, mutated forms of Pyruvate oxidase - having specific aminoacid substitutions, useful as assay reagents, are encoded in new DNA.		
XX			
PS	Claim 15; Page 6; 10pp; German.		
XX			
CC	The sequence of wild-type POD, given below, may be mutated so that at least 178-Pro and/or 425-Ala are exchanged.		
CC	ESP, the mutation is from 178-Pro to Ser and/or 425-Ala to Val.		
CC	The mutated Pyruvate oxidase (POD) decarboxylates pyruvate with formation of H2O2 and is active without addn. of FAD, thiamine pyrophosphate and divalent metal ions. It is more stable (esp. in presence of salts and at alkaline pH) than wild-type enzyme, and is better suited for assay of pyruvate, or pyruvate-generating reactions.		
CC	See also Q08597.		
XX			
SQ	Sequence 570 AA:		
Query Match	17.8%; Score 530.5; DB 11; Length 570;		
Best Local Similarity	26.5%; Pred. No. 3.9c-37;		
Matches	141; Conservative 112; Mismatches 229; Indels 51; Gaps 9;		
Qy	9 LITTLEAQGVKRYIQLGVGDSLNPIVDAY--ROSDIEWVHVRNEAAFAAGAESLINGEL	65	
Db	17 vikvleawgvdnlygipggsinsimdaesaerdihyiqvrheevanahaadakitgk	76	
Qy	67 AVCAASCGFCNTLHQIYDPSHRNGAKVLAIAHSIHSQIQGSFFQEEHPELKECCSY	126	
Db	77 gycfgsagggthmlmglydaredhypvallgqftgqmdtfgeunnenpyadvd	136	
Qy	127 CEMVNGEGERLILMATAQSTWMAGKGVSVVVFPGDIKEADAGDGTYSNSTISGTPVVF	186	
Db	137 nvtavnaatlpvhvdeairrayahqgravqipvdplpqq-----ipaerpl-	184	
Qy	187 DPTEAAALVVAINNAKSUTLFCGAGVKNRAQVLEAELKIKSPIGHALGGKQVYHQENFF	246	
Db	185 -----yydigarkagkeleqlsktklkipmstypakgivadvrya	224	
Qy	247 EVGMSGLLGYGACVDAASNEADLLLGLDFPNSD--FLPKDNQVAQDINGHIGRFT	302	
RESULT	3		
ID	R05793		
XX			
AC			
DT			
XX			
DE	Pyruvate oxidase (wild-type).		
XX			
KW	POD; mutation; decarboxylation; assay.		
OS	Synthetic.		
XX			
PN			
XX			
PD	05-APR-1990.		
XX			
PF	88DE-3833601.		
XX			
PR	03-OCT-1988;	88DE-3833601.	
XX			
PA	(BOEFL) BOEHRINGER MANNHEIM GMBH.		
XX			
PI	Mollerling H, Schumacher G;		
XX			
DR	WPI: 1990-108586/15.		
XX			
PT	New stable, mutated forms of Pyruvate oxidase - having specific aminoacid substitutions, useful as assay reagents, are encoded in new DNA.		
XX			
PS	Claim 15; Page 6; 10pp; German.		
XX			
CC	The sequence of wild-type POD, given below, may be mutated so that at least 178-Pro and/or 425-Ala are exchanged.		
CC	ESP, the mutation is from 178-Pro to Ser and/or 425-Ala to Val.		
CC	The mutated Pyruvate oxidase (POD) decarboxylates pyruvate with formation of H2O2 and is active without addn. of FAD, thiamine pyrophosphate and divalent metal ions. It is more stable (esp. in presence of salts and at alkaline pH) than wild-type enzyme, and is better suited for assay of pyruvate, or pyruvate-generating reactions.		
CC	See also Q08597.		
XX			
SQ	Sequence 570 AA:		
Query Match	17.8%; Score 530.5; DB 11; Length 570;		
Best Local Similarity	26.5%; Pred. No. 3.9c-37;		
Matches	141; Conservative 112; Mismatches 229; Indels 51; Gaps 9;		
Qy	9 LITTLEAQGVKRYIQLGVGDSLNPIVDAY--ROSDIEWVHVRNEAAFAAGAESLINGEL	65	
Db	17 vikvleawgvdnlygipggsinsimdaesaerdihyiqvrheevanahaadakitgk	76	
Qy	67 AVCAASCGFCNTLHQIYDPSHRNGAKVLAIAHSIHSQIQGSFFQEEHPELKECCSY	126	
Db	77 gycfgsagggthmlmglydaredhypvallgqftgqmdtfgeunnenpyadvd	136	
Qy	127 CEMVNGEGERLILMATAQSTWMAGKGVSVVVFPGDIKEADAGDGTYSNSTISGTPVVF	186	
Db	137 nvtavnaatlpvhvdeairrayahqgravqipvdplpqq-----ipaerpl-	184	
Qy	187 DPTEAAALVVAINNAKSUTLFCGAGVKNRAQVLEAELKIKSPIGHALGGKQVYHQENFF	246	
Db	185 -----yydigarkagkeleqlsktklkipmstypakgivadvrya	224	
Qy	247 EVGMSGLLGYGACVDAASNEADLLLGLDFPNSD--FLPKDNQVAQDINGHIGRFT	302	
RESULT	4		
ID	W22459	standard; Protein: 562 AA.	
XX			
AC	W22459;		
XX			
DT	25-SEP-1997 (first entry)		
XX			
DE	E. coli acetolactate synthase isozyme I (sub-sequence E).		
XX			
KW	Acetolactate synthase; ALS; herbicide resistance; transgenic plant; crop protection.		
XX			
OS	Escherichia coli.		
XX			
PN	US5605011-A.		
XX			
PD	25-FEB-1997.		
XX			
PF	86US-0900609.		
XX			
PR	27-JUL-1997; 871L-0083348.		
XX			
PA	(DUPO) DU PONT DE NEMOURS & CO E I.		
XX			
PI	Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;		
PI	Yadav NS;		
XX			
DR	WPI: 1997-153232/14.		
XX			
PT	use of mutant acetolactate synthase genes - for transforming plants for resistance to sulphonylurea, triazolopyrimidine sulphonamide and imidazolinone herbicides.		
XX			
PS	Claim 1; Fig 6a-f; 63pp; English.		
XX			
CC	Amino acid sub-sequences A-G respectively correspond to the large subunits of acetolactate synthase (ALS) isozymes I, II and III (W22459-61) from E. coli, and wild-type ALS proteins of yeast (W22458), Arabidopsis thaliana (W22457) and tobacco (W22455 and W22456). Comparison of these substantially conserved sequences with those of herbicide-resistant ALS enzymes (see also W22462-64) reveal the location of amino acid substs. that lead to herbicide resistance. In sub-sequence E, such a substn. is located at the gamma-1 position (any amino acid other than aspartic acid). A nucleic acid encoding an ALS from any source can be mutated so that the encoded enzyme contains this amino acid substn. Transformation of herbicide sensitive plants or plant cells with the nucleic acid results in resistance to the herbicide.		
CC	Sequence 562 AA;		

Query Match		Score	522.5;	DB	18;	Length	562;
Best Local Similarity		28.1%	pred. No.	1.9e-36;	Mismatches	239;	Indels
Matches		163;	Conservative	107;	Matches	163;	Gaps
QY	6 AEQOLIDTLEAQVAKRIVYLVGDSLNPVDAVROS-DIENWHRNEAAFAAGAESLITG	64	65 ELAVCAASCGPGNHLQIQLGQDLSHRNGAKVLAASHPSAQESTSTFFOEMHPEILFKCS	64	QY	65 ELAVCAASCGPGNHLQIQLGQDLSHRNGAKVLAASHPSAQESTSTFFOEMHPEILFKCS	64
Db	16 aefivhfliegqgkivtqigpgsllpvysdalsstqrlhilarheqgqfiaggardq	75	76 kpvcmacsgpgtnlvtaidardlsiplicitqgvbasmitgtdafqevdyqisipit	135	QY	76 kpvcmacsgpgtnlvtaidardlsiplicitqgvbasmitgtdafqevdyqisipit	135
QY	125 GYCEMVNGGEEQGERILHHAQSTMAGK-GWSVVVIPGDI-----AKEDAGDT	171	136 khylvrhieelpqmsdafridaqsgppqpwidpkvqavfieqtqpmakaapa	195	QY	136 khylvrhieelpqmsdafridaqsgppqpwidpkvqavfieqtqpmakaapa	195
QY	172 YSNSTISGTPVVFDPTEAAVLAIVEATTANAKSVTLCGAGVKAQAVIQLAEIKSPIC	231	232 HALGGKQVIQHENPFEVGMSGLLGYGACVDAVASNEADLILIGTDF-----PYSDFLPKD	285	QY	232 HALGGKQVIQHENPFEVGMSGLLGYGACVDAVASNEADLILIGTDF-----PYSDFLPKD	285
Db	242 intimalgmpkaphlslqmgmhpvrstnuylqeadllivlgarfdrraigktqegfcplia	301	242 intimalgmpkaphlslqmgmhpvrstnuylqeadllivlgarfdrraigktqegfcplia	301	QY	242 intimalgmpkaphlslqmgmhpvrstnuylqeadllivlgarfdrraigktqegfcplia	301
QY	286 NVAQDINGAHIGRTTVKYP-----VTGDAVATIENILPIKEKTDRSFLDRMLKAHERK-	341	302 kihvdidqaglk---1kphvaiqadidvilaqlipv-eaqprawhqlvdalqref	357	QY	302 kihvdidqaglk---1kphvaiqadidvilaqlipv-eaqprawhqlvdalqref	357
Db	342 --LSSVWEMYTHAVKEKHPVHPEYVASINELLA---DKDAVFTWDTCMNCVNHARY-T	393	342 --LSSVWEMYTHAVKEKHPVHPEYVASINELLA---DKDAVFTWDTCMNCVNHARY-T	393	QY	342 --LSSVWEMYTHAVKEKHPVHPEYVASINELLA---DKDAVFTWDTCMNCVNHARY-T	393
Db	358 pcippkacdpfslh-----ylinavracvdanaiittdvgghqmwtaqaypl	404	394 ENPGTRDFWGSFRHGTMANALPHAIGAQSVDRNQVITAMCGDGGLGMGLIGELLTVKHQ	453	QY	394 ENPGTRDFWGSFRHGTMANALPHAIGAQSVDRNQVITAMCGDGGLGMGLIGELLTVKHQ	453
Db	405 npr---rqwtstsgqglgtungfqlpaaigaalanpdtkvlfcsqgdslmmniqematasenq	461	405 npr---rqwtstsgqglgtungfqlpaaigaalanpdtkvlfcsqgdslmmniqematasenq	461	QY	405 npr---rqwtstsgqglgtungfqlpaaigaalanpdtkvlfcsqgdslmmniqematasenq	461
Db	454 LPLKAVVFNNSLGMV-KLEMVLEQPEF-GTDMEVNFIAEIAAAGINSVRIIDPKKR	511	462 ldkvilmnealglvhqgqslfyeqgafavtqpgkqnfmliaangfglecdlnneadpq	521	QY	462 ldkvilmnealglvhqgqslfyeqgafavtqpgkqnfmliaangfglecdlnneadpq	521
Db	512 EQLEALAYPGPVLDIVDTPNAL---SITPTITWEQWMG	548	512 EQLEALAYPGPVLDIVDTPNAL---SITPTITWEQWMG	548	QY	512 EQLEALAYPGPVLDIVDTPNAL---SITPTITWEQWMG	548
Db	522 aslqeiniqpgpalihvridaekvypmwPpgaaanteimq	561	522 aslqeiniqpgpalihvridaekvypmwPpgaaanteimq	561	QY	522 aslqeiniqpgpalihvridaekvypmwPpgaaanteimq	561
RESULT	5						
P81153							
ID	P81153 standard; protein; 562 AA.						
AC	AC						
XX	P81153;						
XX							
DT	17-OCT-1990 ( first entry)						
DE	Herbicide sensitive, wild type ALS.						
XX							
KW	Tobacco; C3 mutant; SURA; acetolactase synthase; sulphonylurea herbicide						
OS	Arabidopsis thaliana.						
XX							
PN	EP237993-A.						
XX							
PD	02-MAR-1988.						
XX							
PF	20-AUG-1987; 87EP-0307384.						
XX							
PR	26-AUG-1986; 86US-0900609.						
XX							
PA	(DUP0 ) DU PONT DE NEMOURS CO.						
PI	Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Yadav NS;						
XX							
XX	WPI: 1988-058164/09.						
XX							

PT	New nucleic acid fragment coding - for mutant aceto-lactate
PR	subtilase resistant to sulphonyl-urea herbicides, and
XX	transgenic plant.
PS	Disclosure: ; P; English.
CC	The sequence is that of the wild type herbicide sensitive form of ALS
CC	encoded by the SURA gene.
CC	See also P81149-55.
XX	
SQ	Sequence 562 AA;
RESULT	6
W22460	W22460 standard; Protein: 548 AA.
XX	
XX	W22460;
XX	
XX	25-SEP-1997 (first entry)
XX	
DE	E. coli acetylactate synthase isozyme II (sub-sequence F).
XX	
XX	Acetylactate synthase; ALS; herbicide resistance; transgenic plant;
XX	crop protection.
XX	
OS	Escherichia coli.
DB	Query Match 17.3%; Score 517.5; DB 9; Length 562;
DB	Best Local Similarity 27.9%; pred. No. 5e-36;
DB	Matches 162; Conservative 107; Mismatches 240; Indels 71; Gaps
QY	6 AEQLIDLTLEQGVKRVIGVYGLGDSLNPIVDAVROS-DIEWVWIVRNEEAFAAGAESLITG 64
QY	16 aeflvinfldeggikivtgipggsilpbydalsqstqnhilarhedgagfaqgmaatdg 75
QY	65 ELAVCAASCGPNTHLQGLYDSHRNGAKVLAISHPSAQGSTFQETHBLFBCS 124
DB	76 kpvomacsgpqtalivatadaridlsiplicitqgypasmigtdaqfegdyqisip 135
QY	125 GYCEMNGEGERILHHAUTSMACK-GVSVWVIREGID-----AKEDAGFT 171
DB	136 khnyvrhieelpqvsndaffiaqsgsrgpwpwidpkdqvtafeletqpanaekasaapa 195
QY	172 YSNSTISSLGIPVWFPDPTEAALVEINNAKSUTLPCGAGVNARAOYVLEAKIKSBRG 231
DB	196 fseesi-----fdaaam--Inaakipvly1999vnaparvrelaekaqptt 241
QY	232 HALGKQVQIHENPFEVGMSGULGIGACVDASENADILLIUGTDF-----PSDFLPKID 285
DB	242 mtlimalqmlpkahtps1qmlgmgmrvstny1lqeadlilivgarfdnraighteqcpna 301
QY	286 NVAQDINGANIGRRTVKY-----VFGDVAITENILPHVKEKTDRLDMKAHEK- 341
DB	302 kihvdidraqlgk--ikqphvaqadddvilaqlipv-eaqprawhqlvadqlref 357
QY	342 ---LSVWVETYTHNVERKHPVHPEYVAVSTLNELA---DKDAVFTVDIGMCNTWHARY--I 393
DB	358 pepikacdpish-----yqilinavaacavdnaalittdvgqhqmtaqaypl 404
QY	394 ENPEGTRDFVGCSFRHGTMANALPHAGAQSVDRNRQVITAMCDGGILGMLGEILTVKHQ 453
DB	405 nrp---rqwitssgg1gmgfcpaatgaalanpldrkviclfsgdslnnniunqematasenq 461
QY	454 LPLKAVVFNNSLGLM-KLEMIVEGQPF-GRDHEEAFRMAAGKSVRITDPKKWR 511
DB	462 ldkvklmnnnealglvhqqs1fyedgafavatygkfinfmqiaagfietcdinneadpq 521
QY	512 EQKAPALAVYGVGPVLIDIVTDNAL--SIPPTIWEGWNG 548
DB	522 aslqlelinrpqpalihvridaeekvyybmvppgaantemng 561

PN	US5605011-A.	Db	404	gfglpaavqavarpnadvicisgdgsfmmvngelgtvkqkqlpkivldnqrlmvrq
XX		XX	472	EMLVECGPEFG---TQEHEVNFAETAAGAGTSKSRVTPKVKVREQLAEALAYPGPVLI
PD	25-FEB-1997.	QY	527	521
XX		Db	464	wqqifderyseytltlonpd--fmlasafqglnghqtrkveaaldmhsdgpylhl
PR	27-JUL-1987;	QY	528	IVTD 531
XX	(DUPO ) DU PONT DE NEMOURS & CO E I.	Db	522	vsid 525
PA				
XX	Bedbrook JR, Chaleff RS, Falco SC, Mazur BJ, Somerville CR;			
PT	PT			
Yadav NS;	XX			
DR	WPI; 1997-153232/14.			
XX				
PT	Use of mutant acetolactate synthase genes - for transforming plants			
PT	for resistance to sulphonylurea, triazolopyrimidine sulphonamide			
PT	and imidazolinone herbicides.			
XX				
PS	Claim 1; Fig 6a-f; 63pp; English.			
XX				
CC	Amino acid sub-sequences A-G respectively correspond to the large			
CC	subunits of acetolactate synthase (ALS) isozymes I, II and III			
CC	(W22459-61) from E. coli, and wild-type ALS proteins of Yeast			
CC	(W22458). Comparison of these substantially conserved sequences			
CC	with those of herbicide-resistant ALS enzymes (see also W22462-64)			
CC	reveals the location of amino acid substrs. that lead to herbicide			
CC	resistance. In sub-sequence F, such substrs. are located at the			
CC	beta-3 (any amino acid other than tryptophan) and beta-7 (any			
CC	amino acid other than phenylalanine) positions. A nucleic acid			
CC	encoding an ALS from any source can be mutated so that the encoded			
CC	enzyme contains these amino acid substrs. Transformation of			
CC	herbicide sensitive plants or plant cells with the nucleic acid			
XX	results in resistance to the herbicide.			
SO	Sequence 548 AA;			
Query Match	17.3%	Score	515;	DB 18; Length 548;
Best Local Similarity	30.1%	Pred.	No. 7.9e-36;	
Matches	164;	Mismatches	91;	Indels 40; Gaps 13;
QY	6 AEQLIDTLEQGVKRIVGLVGDSLNPIVDVARQSDIEWVHVNNEAAFAAGAESLTGE	Db	404	gfglpaavqavarpnadvicisgdgsfmmvngelgtvkqkqlpkivldnqrlmvrq
Db	4 aqwwvhalaqqvntvfgypgqaimpydyldggvhehlcrrheqgaaalgyaratgk	XX	472	EMLVECGPEFG---TQEHEVNFAETAAGAGTSKSRVTPKVKVREQLAEALAYPGPVLI
QY	66 LAVCMASCGPENTHLIQLGDSHRSNAKVLIAHSHTPSAQTSQGTSFFOETHEPEILIRECSG	XX	527	521
Db	64 tgvciatsgqatnltgladalsipvvaltgqasapfqtgdafqevavglslactk	XX	464	wqqifderyseytltlonpd--fmlasafqglnghqtrkveaaldmhsdgpylhl
QY	126 YCEMVNGGEGERTILHAIQSTMDRK-GVSVWVPGDIKEADAGBQTYSTISSTGTPV	XX	528	IVTD 531
Db	124 hsfvlvslsleelprlmaeaefdavcaspqpvapipdi-lasgldepwfttven-tvt 180	XX	522	vsid 525
QY	185 FPPPTENALVALVEINNAKSVLFCGKGKVNRA---QVLELAEKIKSPIGHALKQVQH	XX		
Db	181 fph-aseveqarqmlakqakpmlqyggqgqapalprefaaatkmpatctlkqigavea	XX		
QY	243 ENPFEGVMSGLGILGYGACVDAVSNEADILLGLTF-----PYSDFLPKDNVAQVDINGAH	XX		
Db	240 dypyyvlqmlgmgktkaanfaqvcdllawgarfadrvlgklntraphasvihmidpae	XX		
QY	297 IGRRT"VVKVPPVQGDAVATENILPHKEKTDRLDRFLDRMLKAHERKUSSVVTYTYNEVKH	XX		
Db	300 mnk1rqahvalqdgdnalp1qspinqydwqhqcaqrdrhswr-----ydh-----347	XX		
QY	357 VPIIPEPVVASTLNELADK---DAVFTVDTGKCNVNHARYTEN---PECTRDPVGSRHGTW	XX		
Db	348 -pgdalyapllkq1sdkrpdcvvttdvqghqmaaqhiahtripe--nfttssqigtm	XX		
QY	412 ANALPHAIAGQASVDRNRRQVAMCGDGGLGMULGELITVKUHQPLPKAVVNNSLGMVKL	XX		
Db	4 aqwwvhalaqqvntvfgypgqaimpydyldggvhehlcrrheqgaaalgyaratgk	XX		
Query Match	17.2%	Score	514;	DB 17; Length 548;
Best Local Similarity	30.1%	Pred.	No. 9.6e-36;	
Matches	164;	Mismatches	91;	Indels 40; Gaps 13;
QY	6 AEQLIDTLEQGVKRIVGLVGDSLNPIVDVARQSDIEWVHVNNEAAFAAGAESLTGE	Db	404	gfglpaavqavarpnadvicisgdgsfmmvngelgtvkqkqlpkivldnqrlmvrq
Db	4 aqwwvhalaqqvntvfgypgqaimpydyldggvhehlcrrheqgaaalgyaratgk	XX	472	EMLVECGPEFG---TQEHEVNFAETAAGAGTSKSRVTPKVKVREQLAEALAYPGPVLI







CC	the gene can thus be used to provide crop plants with resistance
CC	to herbicides such as imidazolinones, triazolopyrimidines and
CC	sulphonylureas. See also R24798-R24801 and R28609-R28624.
XX	
SQ	Sequence 669 AA:
Query Match	16.6%; Score 495.5; DB 13; Length 669;
Best Local Similarity	27.4%; Pred. No. 5.1e-34;
Matches	157; Conservative 96; Mismatches 261; Indels 59; G
QY	
6	AEQDITLEQEVKRYGLGDSLNPIVDVAWSQDIEWYHVRNEAAAPAGAESLTIGEE
Db	100 aolivcalerqvetvraypgasmehqalttrssirnvprheggvraeagyarsggk
QY	66 LAVCASCAGCANTHILQGLYDLSHRNGAKVIAASHIPSQKIGSTPFOEHTHEPELIFKECSGG
Db	160 pgciatssggatnivsgiadollspivaltqgvprmrigdcafetpivevtsitk
QY	126 YCEMVNGCEROCERTLHATOSTMACK-GSVVWPGDTAKEDAGDGTVNSTISGGTPVV
Db	220 hnylvindvedaprlteafatlatsgrgppvlpvdwpkdl-qcqqlalpnwqgamtlpqyinrr
QY	185 FPDPEVAAAL---VIAINNAKSVVLFCGAGVKNAQVLELAEKIKSPIGHALGGKQVIQ
Db	279 mpkppedsh1eqivrliscckkpvlyvsggclnsdelgrfveltgipvastlinggyp
QY	242 HENPPEVGMGSLGLGAGNCVDRSNEADLTLIGTDF----PYSDFLPKDNVAQDINGA
Db	339 cddelshlmymghgtvyanavensdillafgvsfdrtwgkleafastrakivhidas
QY	296 HIGRGRVVKVPTGVQAATENTILPHVKEKTDRLDRML--KAHERKLSVSVETYTHNV
Db	399 elgknktpvhpsvcgavklaq-----mknvlenraeklqfgrwvnelnv
QY	354 EKH-----VPIHPEVAVSTLNEADKDAVFTVGDGMCNWARYIENEGTRPVE
Db	446 qkqkfpisftkfgaippgavakvldeltcgkaklistgvgqhqmaqf-nykkprqwl
QY	404 GSFRGTMALPHALIGAQSVDNRQVIAACGAGLGMILGELITVKHQOLPKAVVNN
Db	505 ssggagmngqqlpaagiasvanpdavridqdggsfimnvqelatirvenlpkvllino
QY	464 SSLGMKMLELVE-----GOREFGTQHEEV--NFAETAAAGIKVTRTPKE
Db	565 qhlgmvs---mnedfrykanrahtflgdp---aqedelppnnllfaaacgipaavrtkk
QY	509 KVREQLAEANAYPGVLLIDVTDNALSPPTI 541
Db	619 dlrealqtmldtpgpy11dovic-phqehvlpml 650
RESULT	13
R28623	
ID	R28623 standard; protein: 669 AA.
XX	
NC	
XX	
XX	
DT	11-DEC-1992 (first entry)
DE	Val1571 deleted acetohydroxy acid synthase.
XX	
KW	NRAS; herbicide resistance; plants; imidazolinones;
KW	triazolopyrimidines; sulphonylureas;
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP492113-A.
XX	
PD	01-JUL-1992.
XX	
PF	12-NOV-1991; 91EP-0119254.

PR	27-DEC-1990;	90US-0633210.
XX		
PA	(AMCY )	AMERICAN CYANAMID CO.
XX		
PT	Chaleff RS, Hand JM, Singh BK;	
XX		
DR	WPI: 1992-218438/27.	
XX		
PT	Aceto-hydroxy acid synthase enzyme deletion mutants - encoded by	
PT	nucleic acid sequences which can confer herbicide resistance to	
PT	plants	
XX		
PS	Claim 4; Page 20; 37pp; English.	
XX		
CC	The sequence is that of Val571 deleted aceto-hydroxy acid synthase	
CC	(AHAS) which is herbicide resistant. Transgenic plants may be	
CC	produced which contain the modified gene and produce the Val571	
CC	deleted AHAS in the presence of an inhibitory amt. of herbicide.	
CC	The gene can thus be used to provide crop plants with resistance to	
CC	herbicides such as imidazolinones, triazolopyrimidines and	
CC	sulphonylureas. See also R24798-R24801 and R28609-R28624.	
XX		
SO	Sequence 669 AA;	
Query Match	16 %;	Score 495.5; DB 13; Length 669;
Best Local Similarity	27.4 %;	DB 13; Length 669;
Matches	156;	Score 495.5; DB 13; Length 669;
Conservative	99;	Score 495.5; DB 13; Length 669;
Mismatches	62;	Score 495.5; DB 13; Length 669;
Indels	53;	Score 495.5; DB 13; Length 669;
Gaps		Score 495.5; DB 13; Length 669;
QY	6 AEQLIDTELEQVKRIVYGLGDSLNPVIAV-ROSDIENWHRVNEEAAFFAACAEPLITG	64
Db	100 adlivelaelegqgevfvafqrgasmeingaltssirnwlprheggvfanegyayssg	159
QY	65 ELAVCAASCCPGNTLHQIQLQYDHSHRNQAKVLTASHPSAQGTSFRTETHPILFBCS	124
Db	160 kpgiciatsggatnvlsgladalldsdpvlavtgcqvprrmgtardetplvtrtsit	219
QY	125 GYCEVNNGGCGERTLHHAQSTMAG-CWSVVVPGDIAKEDAGDGIVNSNISSTGPV	183
Db	220 khnyiVndvdiprieeaffatgsgrppvlpvdkl-qgqlapnweqmrlyps	278
QY	184 VFPDPTEAAL--VEAINNAKSVTLCFGAGVNAARAQVLEAKIKSPIGHALGGQYI	240
Db	279 rmpkppedsilqeqvrlisesskpkvlyqgcinssdelgrfveltgtpvastlmqgsy	338
QY	241 OHENPFEGVGGAGLGLGYGACVADASNEADLILILGDF-----PYSDFLPKDNVAQDING	294
Db	339 pcddelelmlmglmgmtvyanayavehsdilafgvfrddrtvgkleafasrakvhidids	398
QY	295 AHIGRRTWVYKPYVQDVAATIENLPHVKEKTRDSFLDRML--KAHERKLSSVETTHN	352
Db	399 aeigknktphvsvcogdklalqg-----mkvlenraeekldigwrmeln	445
QY	353 VEKH-----VPIHREYVASTLNELAKDAVFTDTGMCNVWHARYIENPEGTRDF	402
Db	446 vqkqkfpifstfkfgeapqyaykvldeltdgkaisctgvgqghmwaqy-nykkprq	504
QY	403 VGSFRHGTMNALHAGQSVDRNQVIAIMCDDGGIQLMIGELITVILQQLPLKAVEN	462
Db	505 lssggjgangfrgibaagasavanpdaivvddggsfimnvgelatirvnenipkvillin	564
QY	463 NSSLMVKLE-----MLVEQCPERFGTDHEEV--NFAELAAAGTKSVRITDPKKVR	511
Db	565 nqhlqmgqvpedrfykanrahftqdp--aaqedelppmltaacgipaavrtkkdr	621
QY	512 EQLAEALAVPGPVLTIDVNDPNALSIPIPTI	541
Db	622 eaiqtmldtpgpylldvic-ppqehvlpml	650
RESULT	14	
R28616	R28616 standard; Protein: 666 AA.	



Qy 125 GYCEMVNGEGEGERILHATOSTMACK-GVSVVWPGDIAKEDACOTYSUSTISSGTPV 183  
 Db khnylvndvedipredipeafflatstgrpgpvivdvpkdl-qqqlainpnwqamrpqyms 278  
 Qy 184 VPPDPPEAAL--VEAINNAKSNTLFCGAGYKARAOVLELAEKIKSPIGHALGGKQYI 240  
 Db 279 rmpkpppedshleqivrliseeskppvlyggclnssdelgrfveltgiprastlmgly 338  
 Qy 241 QHENPFEVGMGLLGYACVVDASNEADLTLITGTD-----PYSBRLPKDNVAQDING 294  
 Db 339 pcdeelshmlqmgltvyanayavensdllafrvrtgkleafasrakvhids 398  
 Qy 295 AHIGRRRNUVKPVGVAATENILHVKEKUDRSFLDRM--KAFERKLUSSWEDYTHN 352  
 Db 399 aelgnkntphvavcavklaiq-----mnkvlenraeeklqdgwvnein 445  
 Qy 353 VEKH-----VPIHPEVASILNEADKDAVTVDGMCNVHARVYENPEGRDF 402  
 Db 446 vqkqkfpplsftfgeaippqyavikvideltdgkallstgqyqghqwaqfy-nykppqw 504  
 Qy 403 VGSFRHGTMANALPHITGAQSVDRNQVITAMCGDGGIGMLIGELLTWKLHOLPLKAVVN 462  
 Db 505 lssgg1gagmfglaaigasvandpalvvvdldgdsfilmvqelatirvenlpkvlln 564  
 Qy 463 NSSLGAVKLEMVEGPEFGCDH-----EV--NFAETAAAGIKSRYTDPKKVR 511  
 Db 565 nqhlgnv--nqkwykanrahtflgpaqedelipmnlfaaacgiparvtkadr 621  
 Qy 512 EQLAELAYPGPVLDIVTDNALSLPPTI 541  
 Db 622 eaiqtqndtpqpylidvic-phqehv1pm1 650

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 Job time: 5109 sec

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